



PATENT  
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

Thomas GINGERAS *et al.*

Application No.: 09/285,306

Filed: April 2, 1999

For: MYCOBACTERIAL RpoB SEQUENCES

Group Art Unit: 1656

Examiner: J. Siew

Commissioner for Patents  
Washington, D.C. 20231

Sir:

AMENDMENT UNDER 37 C.F.R. § 1.111

In response to Final Office Action mailed October 4, 2001, please amend the above-identified application as follows prior to examination:

IN THE SPECIFICATION:

Please replace the paragraph beginning at page 8, line 12 and ending at page 9, line 11 with the following:

-- One example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a